

A

| | | |
|-----|---|-----|
| -51 | <u>MEQRGQKAPAAASGARKRHGPGPREARGARPGLRVPKTLVLVVAAVLLLV</u> | -2 |
| -1 | <u>AESALITQQLAPQQRVAPQQRSSPSGLCPFGHHSIEDGRDCISCKYG</u> | 49 |
| 50 | <u>QDYSTHWEDLLFCLECTRCDSGEVELSPCTTTRNTVCQCEGTFREEDSP</u> | 99 |
| 100 | <u>EMCRKCRGTGCPFGMAVVGDCTFWSDIECVKESGIIIGVTVAAVVLTVAV</u> | 149 |
| 150 | <u>FVCKSLMLNKKVLPYLKSGICSGGGGDPFVDRSSQRPFGAEDNVLMKIVSIL</u> | 199 |
| 200 | <u>QPTQVPEQEMEVOEPAPFTGVNMLSPGESKHLLEPAEAERSQRRLLVPA</u> | 249 |
| 250 | <u>MEGDPTEELRQCFDDFADLVPTDSWEPLMRLGLMDNRIKVAKAAAGHR</u> | 299 |
| 300 | <u>DTLYTMLKQVVKTKGRDASVHTLLDALETGLERLAKQKTEHLLSSGKFM</u> | 349 |
| 350 | YLEGNADSAMS* | 360 |

B

| | | |
|-----|---|-----|
| -63 | <u>MOGVKERFLPLGNSGDRAFRFPDGRGRVRPRTQDGVGNETMARIPKTLK</u> | -14 |
| -13 | <u>VVVIVAVLLPVLAISATTARQEEVPQQTVAPOQRHSFKGECCPAGSHRS</u> | 37 |
| 38 | <u>EHTGACNPECTEGVDYTNASNNKPSCTPCTVCKSDQKHKSSCTMTTRDTVCQ</u> | 87 |
| 88 | <u>CKEGTFNNNSPEMCRKCSRCPSGEVQVSNCTSWDDIQCVKEFGANATVE</u> | 137 |
| 138 | <u>TPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAE</u> | 187 |
| 188 | <u>ETMTTSPGTPAPAAETMTTSPGTPASSHYLSCTIVGLIVLIVLIVFV*</u> | 236 |

C

| | | | |
|--------|-----|---|-----|
| DR5 | 273 | <u>SWEPLMRKGLMDNRIK.VAKAAAGHRDTLYTMLKQVVKTKG.RDAEVEH</u> | 320 |
| DR4 | 356 | <u>SWDQLMRQL LTKNEID.VVRAGTAGFGDALYAMLMKQVVKTKG.RNASTH</u> | 403 |
| DR3 | 346 | <u>RHKKEEVRTTGLREAEKLEAVEVEIGH.FPDQOXEMDKRHRQQQP...AGLG</u> | 391 |
| TNFR-1 | 330 | <u>RHKKEEVRTTGLREAEKLEAVEVEIGH.FPDQOXEMDKRHRQQQP...AGLG</u> | 379 |
| FAS | 228 | <u>QVKGEDKQKGVMEAKLIDELKQNVQDTAEQKVQLGRNHBQLHGKKEA.YD</u> | 276 |
| CAR1 | 269 | <u>EMAREGHALDQDQENDLY.LAEQHDVSCPEFYOMLNTWLNQQG.SKAEVN</u> | 313 |
| DR5 | 321 | <u>TEGDAGETLGERLAKQKTE</u> | 339 |
| DR4 | 404 | <u>TEGDAGETLGERLAKQKTE</u> | 422 |
| DR3 | 392 | <u>AVYAKETRMGGGQCVLR</u> | 410 |
| TNFR-1 | 380 | <u>LDGRVLRDMOILGCEDETE</u> | 398 |
| FAS | 277 | <u>TEGDAGETLGERLAKQKTE</u> | 293 |
| CAR1 | 314 | <u>TEGDAGETLGERLAKQKTE</u> | 333 |

FIGS. 1A-C

D

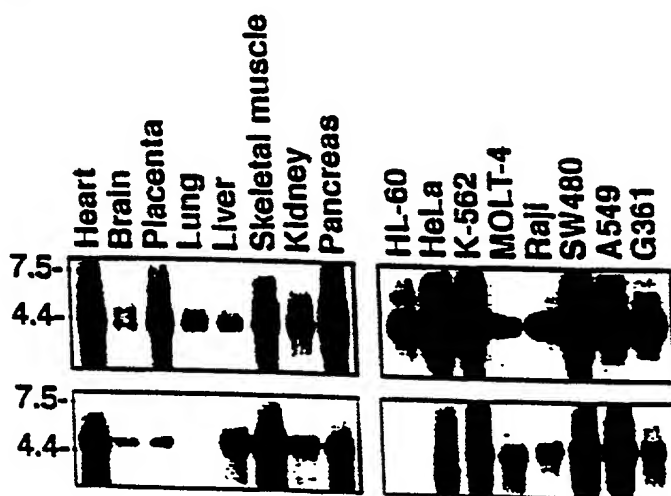


FIG. 1D

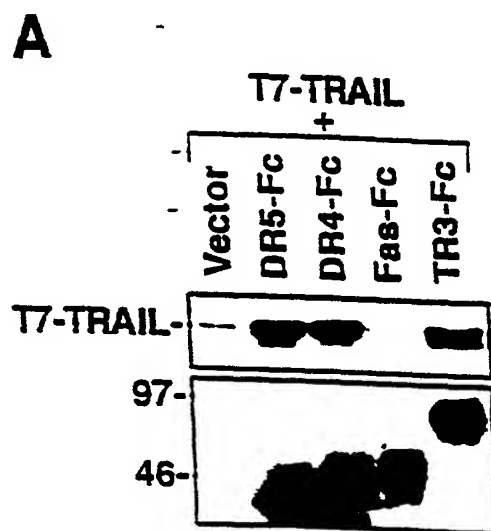


FIG. 2A

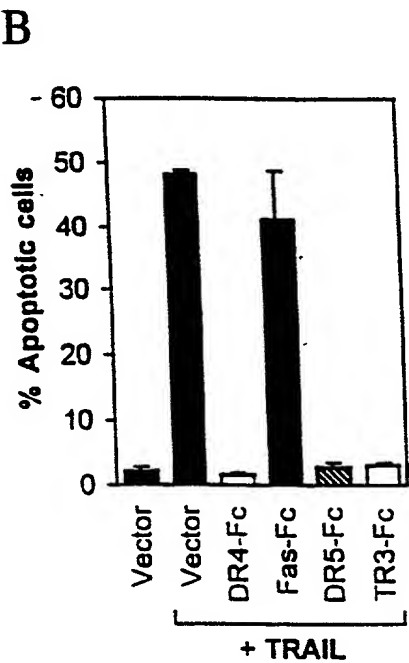
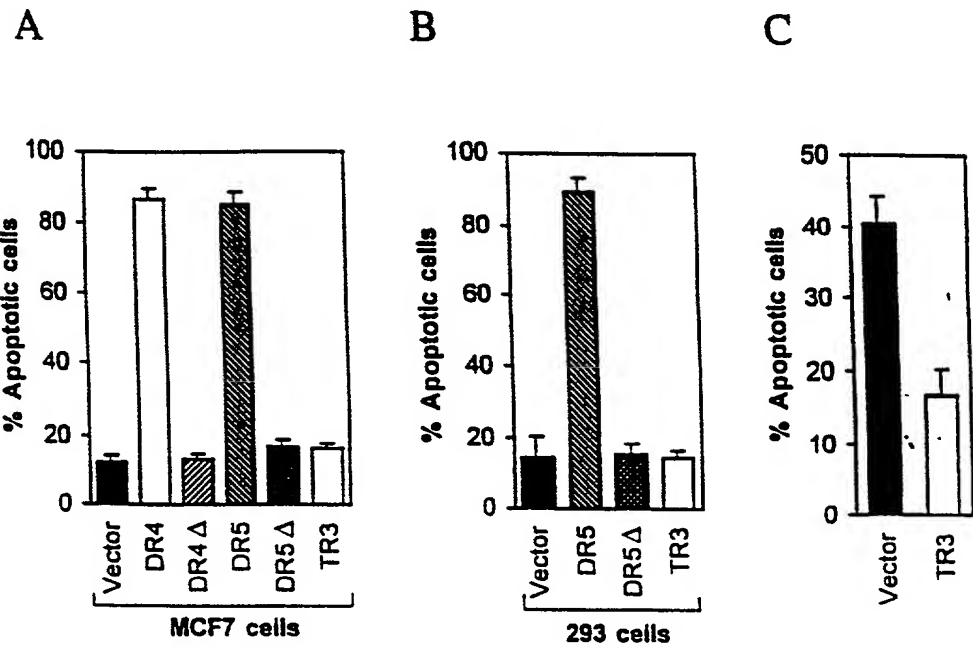
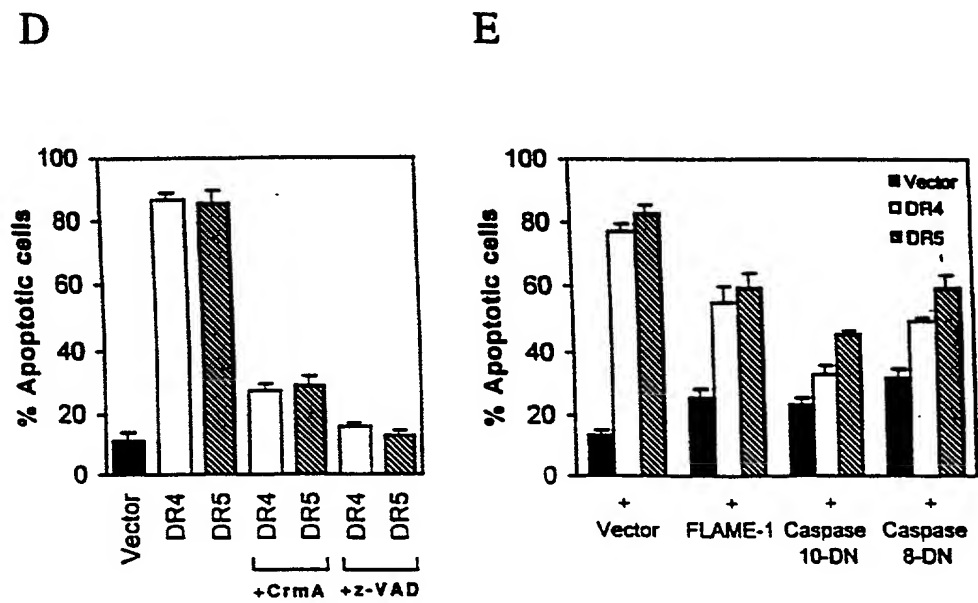


FIG. 2B



FIGS. 3A-C



FIGS. 3D-E

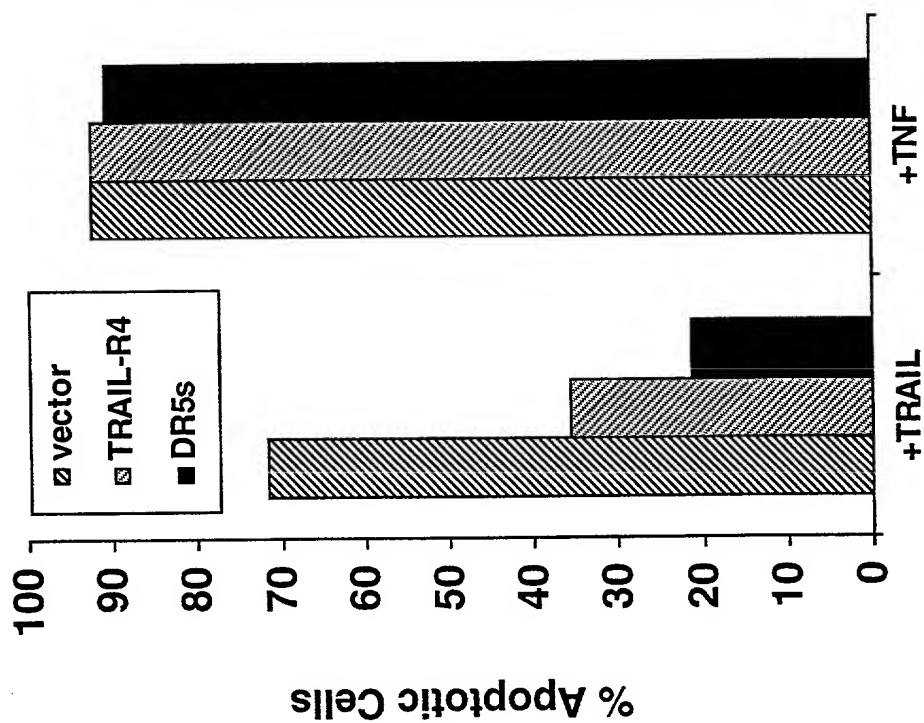
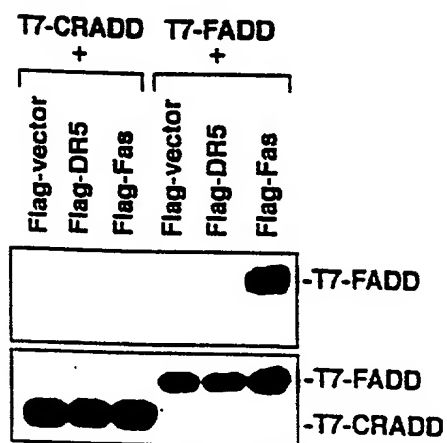
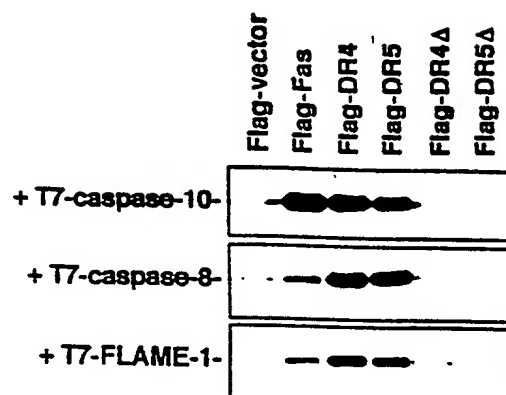


FIG. 3F

A



B



FIGS. 4A-B

1 ATGGAACAACGGGGACAGAACGCCCCGGCCGCTTCGGGGGGCCCGAAAGGCACGGCCCA 60
 1 M E Q R G Q N A P A A S G A R K R H G P 20

61 GGACCCAGGGAGGCGCGGGGAgCCAGGCCTGGGCTCCGGGTCCCCAAGACCCTTGTGCTC 120
 21 G P R E A R G A R P G L R V P K T L V L 40

121 GTTGTGCGCCGGTCTCTGCTGTTGGTCTCAGCTGAGTCTGCTCTGATCACCCAACAAGAC 180
 41 V V A A V L L L V S A E S A L I T Q Q D 60

181 CTAGCTCCCCAGCAGAGAGTGGCCCCACAACAAAAGAGGTCCAGCCCTCAGAGGGATTG 240
 61 L A P Q Q R V A P Q Q K R S S P S E G L 80

241 TGTCCACCTGGACACCATATCTCAGAAGACGGTAGAGATTGCATCTCCTGCAAAATATGGA 300
 81 C P P G H H I S E D G R D C I S C K Y G 100

301 CAGGACTATAGCACTCACTGGAATGACCTCCTTTTCTGCTTGGCTGCACCAAGTGTGAT 360
 101 Q D Y S T H W N D L L F C L R C T R C D 120

361 TCAGGTGAAGTGGAGCTAAGTCCCTGCACCACGACCAGAAACACAGTGTGTGAGTGCAGAA 420
 121 S G E V E L S P C T T T R N T V C Q C E 140

421 GAAGGCACCTTCCGGGAAGAAGATTCTCCTGAGATGTGCCGGAAGTGCCGCACAGGGTGT 480
 141 E G T F R E E D S P E M C R K C R T G C 160

481 CCCAGAGGGATGGTCAAGGTCGGTGATTGTACACCCTGGAGTGACATCGAATGTGTCCAC 540
 161 P R G M V K V G D C T P W S D I E C V H 180

541 AAAGAATCAGGTACAAAGCACAGTGGGAAGCCCCAGCTGTGGAGGAGACGGTGACCTCC 600
 181 K E S G T K H S G E A P A V E E T V T S 200

601 AGCCCAGGGAAGTCTGCCTCTCCCTGTTCTCTCTCAGGCATCATCATAGGAGTACAGTT 660
 201 S P G T P A S P C S L S G I I I G V T V 220

661 GCAGCCGTAGTCTTGATTGTGGCTGTGTTGTTTGAAGTCTTTACTGTGGAAGAAAGTC 720
 221 A A V V L I V A V F V C K S L L W K K V 240

721 CTTCTTACCTGAAAGGCATCTGCTCAGGTGGTGGTGGGACCCTGAGCGTGTGGACAGA 780
 241 L P Y L K G I C S G G G G D P E R V D R 260

781 AGCTCACAACGACCTGGGGCTGAGGACAATGTCCTCAATGAGATCGTGAGTATCTTGCAG 840
 261 S S Q R P G A E D N V L N E I V S I L Q 280

841 CCCACCCAGGTCCCTGAGCAGGAAATGGAAGTCCAGGAGCCAGCAGAGCCAACAGGTGTC 900
 281 P T Q V P E Q E M E V Q E P A E P T G V 300

901 AACAAAACCGGGGAgATGCCTCTGTCCACACCCTGCTGGATGCCTTGGAGACgCTGGGA 960
 301 N K T G R D A S V H T L L D A L E T L G 320

961 gAgAgACTTGCCAAGCAGAAGATTGAGGACCACTTGTGTGAGCTCTGGAAAGTTCATGTAT 1020
 321 E R L A K Q K I E D H L L S S G K F M Y 340

1021 CTAGAAGGTAATGCAGACTCTGCCATGTCCTAA 1053
 341 L E G N A D S A M S * 351

FIG. 5

FIG. 6